MATCHES"

Applicant: Jacques COLINGE et al. U.S. Application No: Not yet assigned. Attorney Docket No.: 62679.00004

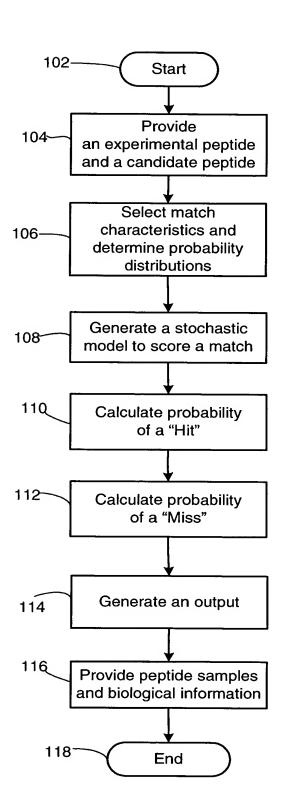


Figure 1

MATCHES"

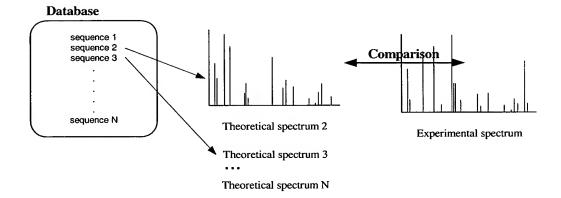


Figure 2a: database search

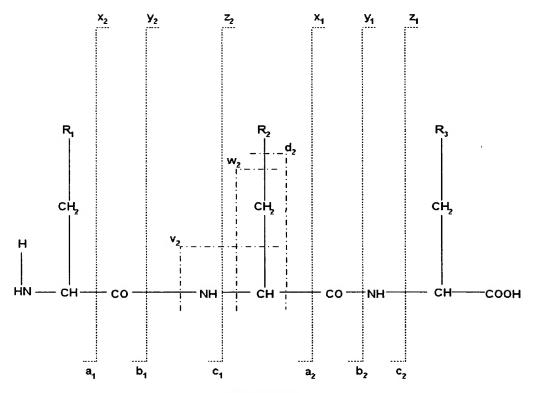


Figure 2b

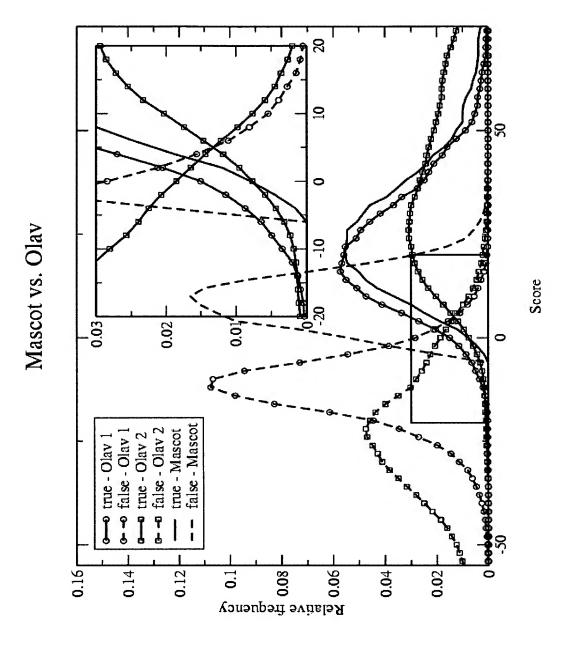


Figure 3

"SYSTEM AND METHOD FOR SCORING PEPTIDE MATCHES"
Applicant: Jacques COLINGE et al.

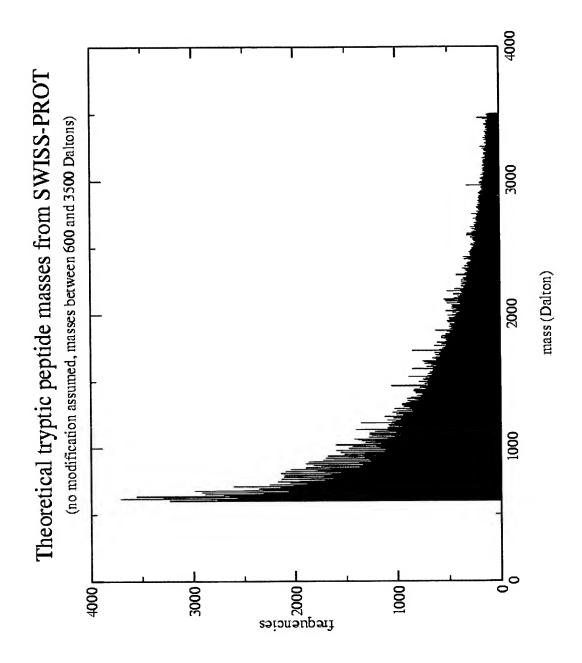
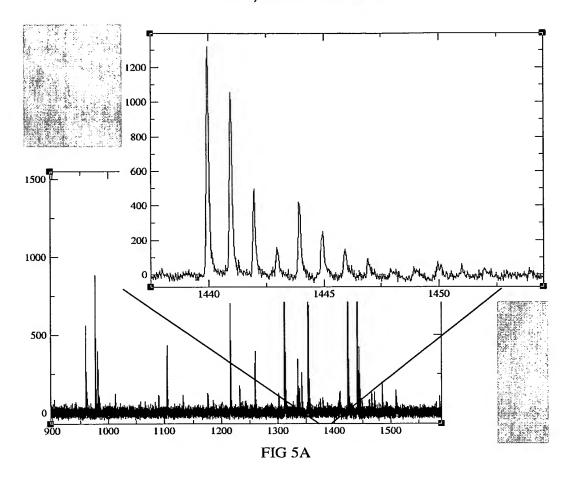
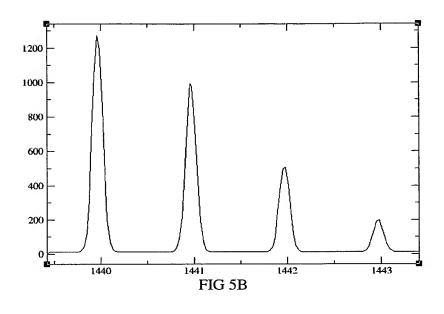


Figure 4





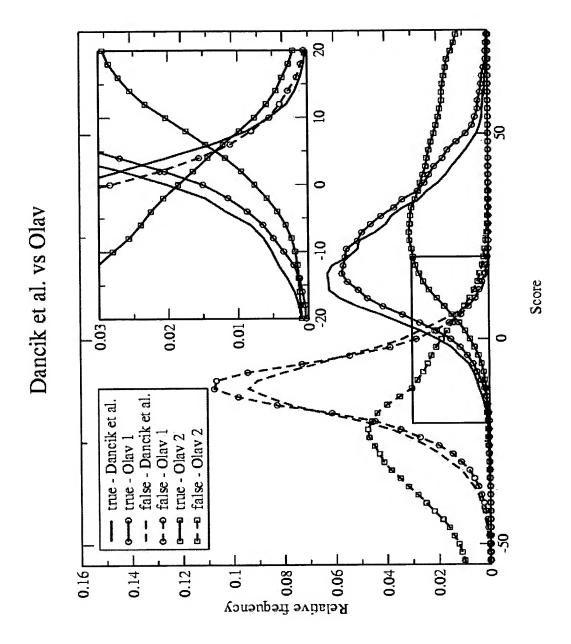


Figure 6

"SYSTEM AND METHOD FOR SCORING PEPTIDE MATCHES"

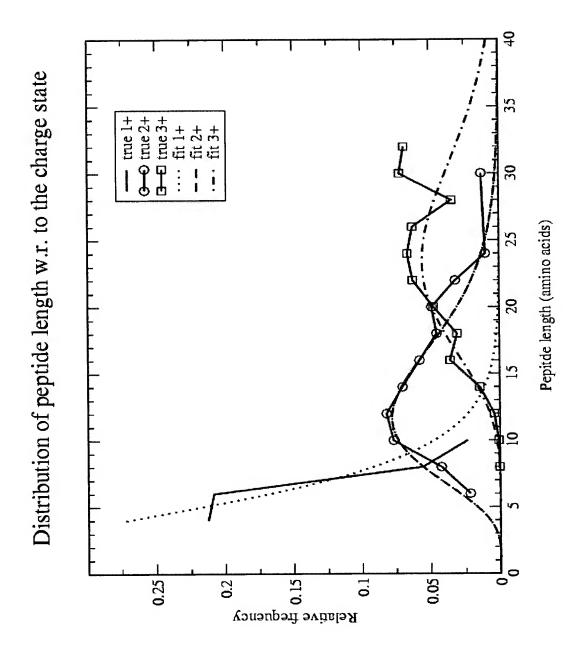


Figure 7

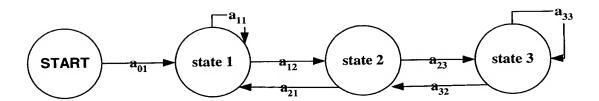


Figure 8

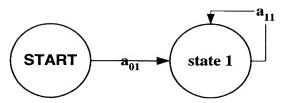
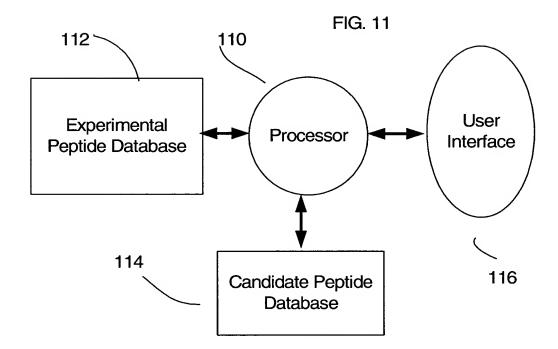


Figure 9: Null model.

a	<u> 000000000000000000000000000000000000</u>
a ll	0
a−H20×	000000000000000000000000000000000000000
	$-\cdot\cdot\cdot\cdot\bulletlack$
	$\underline{}$
a-NH3×	• • • • • • • • • • • • • • • • • • • •
	<u> </u>
Ь	0
ь++	000000000000000000000000000000000000000
b-H20×	000000000000000000000000000000000000000
	· · · · · • • • • • • • • • • • • • • •
	<u> </u>
b-NH3×	\cdot
	<u> </u>
y	<u> </u>
y ++	
y-H20*	000000000000000000000000000000000000
	$ \phi \phi \phi \phi \phi \phi \phi \phi \circ \cdot \cdot \cdot \cdot \cdot \cdot \cdot \cdot \cdot $
	O · · · · · · · · · · · · · · · · · · ·
y-NH3×	-
	<u> </u>

Figure 10

MATCHES"



"SYSTEM AND METHOD FOR SCORING PEPTIDE MATCHES"

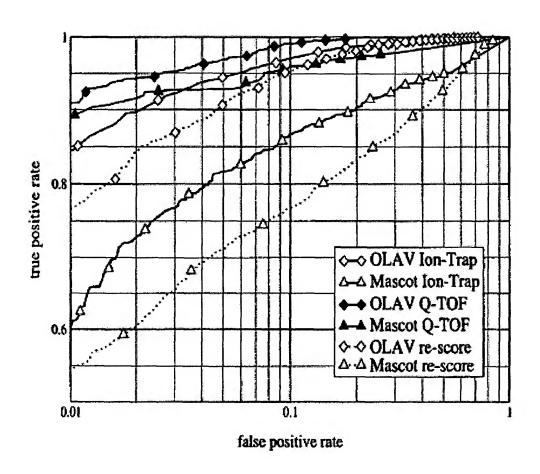


Figure 12

MATCHES"

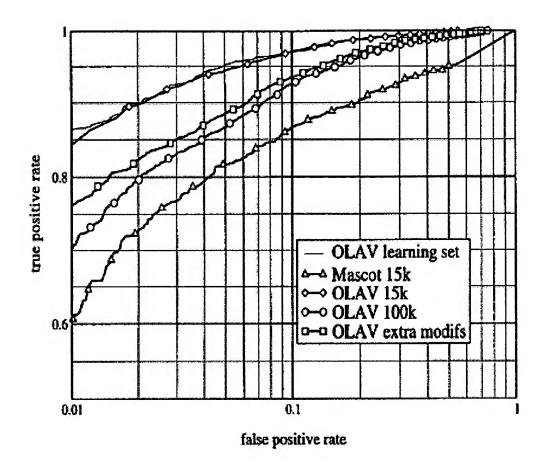
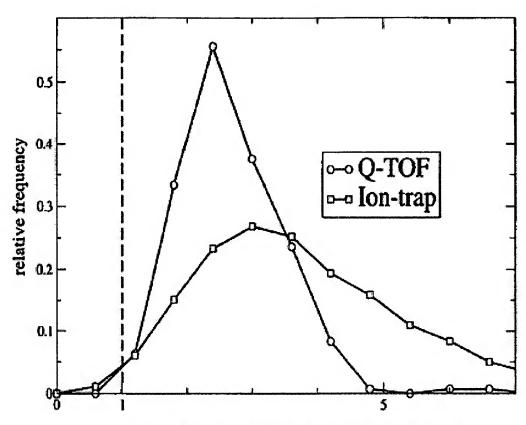


Figure 13



correct match score divided by best random match score

Figure 14

"SYSTEM AND METHOD FOR SCORING PEPTIDE MATCHES"

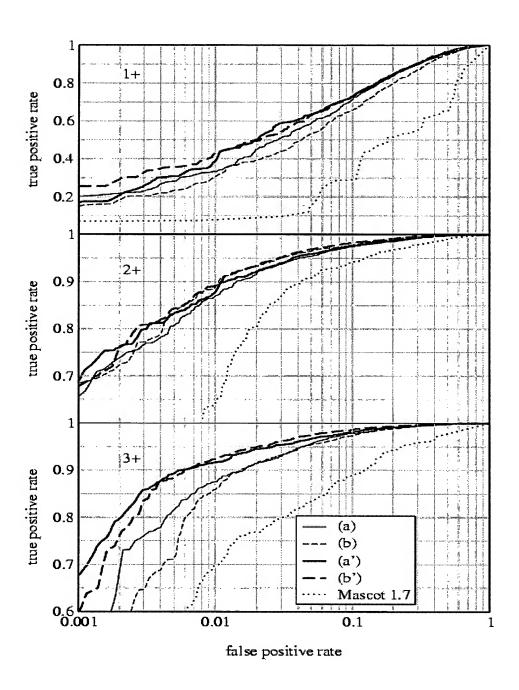


Figure 15

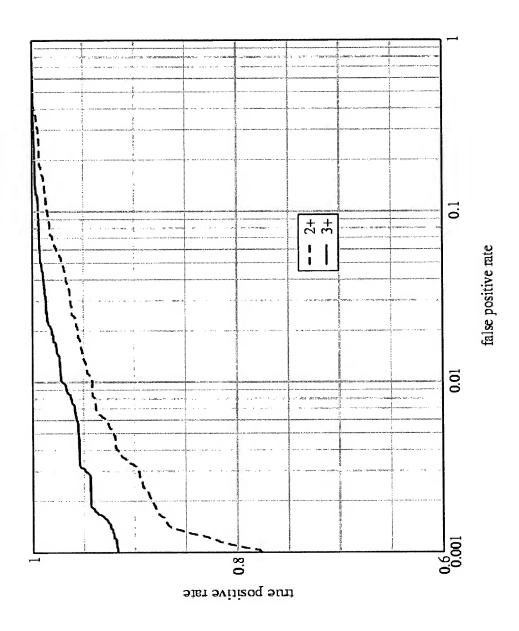


Figure 16

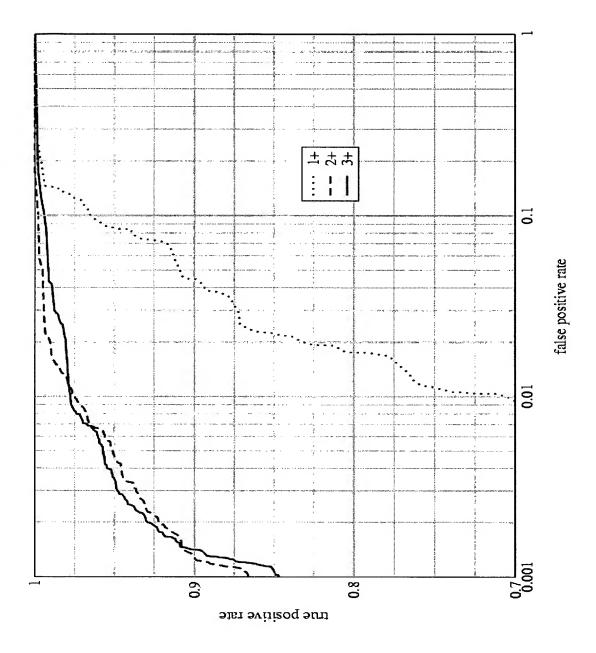


Figure 17

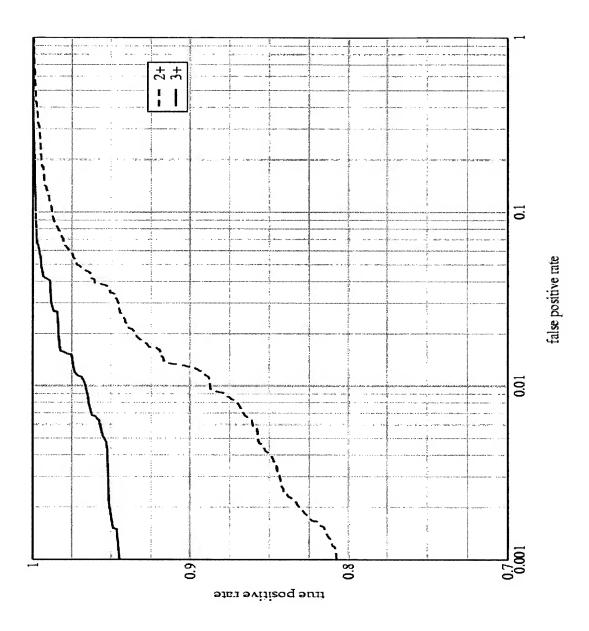


Figure 18